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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=4; day=18; hr=17; min=32; sec=5; ms=354;]

=====

Application No: 10627556 Version No: 3.0

Input Set:

Output Set:

Started: 2009-04-02 18:02:17.053
Finished: 2009-04-02 18:02:36.212
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 159 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

Input Set:

Output Set:

Started: 2009-04-02 18:02:17.053
Finished: 2009-04-02 18:02:36.212
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 159 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520)
W 251	Found intentionally skipped sequence in SEQID (521)
W 251	Found intentionally skipped sequence in SEQID (522)
W 251	Found intentionally skipped sequence in SEQID (523)
W 251	Found intentionally skipped sequence in SEQID (524)
W 251	Found intentionally skipped sequence in SEQID (525)
W 251	Found intentionally skipped sequence in SEQID (526)
W 251	Found intentionally skipped sequence in SEQID (527)
W 251	Found intentionally skipped sequence in SEQID (639)

Input Set:

Output Set:

Started: 2009-04-02 18:02:17.053
Finished: 2009-04-02 18:02:36.212
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 159 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640)
W 251	Found intentionally skipped sequence in SEQID (643)
W 251	Found intentionally skipped sequence in SEQID (646)
W 251	Found intentionally skipped sequence in SEQID (680)
W 251	Found intentionally skipped sequence in SEQID (681)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
W 251	Found intentionally skipped sequence in SEQID (699)

<110> Ledbetter, Jeffrey A.
Hayden-Ledbetter, Martha
Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.401C2

<140> 10627556

<141> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> Homo sapiens

<400> 1

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atctcccgga	cccctgaggt	cacatgcgtg	gtggtggacg	tgagccacga	agaccctgag	180
gtcaaattca	actggtacgt	ggacggcgtg	gaggtgcata	atgccaagac	aaagccgcgg	240
gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtcc	tcaccgtcct	gcaccaggac	300
tggctgaatg	gcaaggagta	caagtgcaag	gtctccaaca	aagccctccc	agcccccatc	360
gagaaaacaa	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	caccctgccc	420
ccatcccgga	atgagctgac	caagaaccag	gtcagcctga	cctgcctggg	caaaggcttc	480
tatcccgagc	acatcgccgt	ggagtgggag	agcaatgggc	agccggagaa	caactacaag	540
accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	gtcaccgtg	600
gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	660
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<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

Ser	Asp	Gln	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
1				5					10					15	
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
			20					25					30		
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			35				40					45			
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
			50			55				60					
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
65					70					75				80	
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
				85					90					95	

Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
			100					105					110		
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
		115					120					125			
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
		130				135					140				
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
145				150						155				160	
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
			165					170					175		
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
		180						185					190		
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
	195					200				205					
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	210					215					220				
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
225				230						235					

<210> 3

<211> 718

<212> DNA

<213> Lama glama

<220>

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<221> modified_base

<222> (43)..(43)

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<222> (52)..(52)

<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (58)..(58)

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<221> modified_base

<222> (64)..(64)

<223> n is a, c, g, or t

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actnccagga	ggcccttctg	tctttgtctt	ccccccgaaa	cccaaggacg	tcctctccat	120
ttttggaggc	cgagtcacgt	gcgtttagt	ggacgtcgga	aagaaagacc	ccgaggtcaa	180
tttcaactgg	tatattgatg	gcgttgaggt	gcgaacggcc	aatacgaagc	caaaagagga	240
acagttcaac	agcacgtacc	gcgtgggtcag	cgctctgccc	atccagcacc	aggactggct	300
gacggggaag	gaattcaagt	gcaaggtcaa	caacaaagct	ctcccgcccc	ccatcgagag	360
gaccatctcc	aaggccaaag	ggcagaccg	ggagccgcag	gtgtacaccc	tggccccaca	420
ccgggaagaa	ctggccaagg	acaccgtgag	cgtaacatgc	ctgggtcaaag	gcttctaccc	480
agctgacatc	aacgttgagt	ggcagaggaa	cggtcagccg	gagtcagagg	gcacctacgc	540

caacacgccg	ccacagctgg	acaacgacgg	gacctacttc	ctctacagca	agctctcggt	600
gggaaagaac	acgtggcagc	ggggagaaac	cttaacctgt	gtggtgatgc	atgaggccct	660
gcacaaccac	tacaccaga	aatccatcac	ccagtcttcg	ggtaaatagt	aatctaga	718

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

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1				5					10					15		
Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	
			20					25					30			
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	
		35					40					45				
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val	
	50					55					60					
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser	
65					70					75					80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu	
			85					90					95			
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala	
		100						105					110			
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro	
	115					120					125					
Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr	
	130				135						140					
Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ala	Asp	Ile	Asn	
145					150					155					160	
Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala	
			165					170						175		
Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser	
		180					185						190			
Arg	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Arg	Gly	Glu	Thr	Leu	Thr	
	195					200						205				
Gly	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
	210					215					220					
Ile	Thr	Gln	Ser	Ser	Gly	Lys										
225					230											

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

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aacagaatcc	aagtgtccca	aatgtccagc	ccctgagctc	ctgggagggc	cctcagtctt	120
catcttcccc	ccgaaccaca	aggacgtcct	ctccatttct	gggaggcccg	aggtcacgtg	180
cgttgtggta	gacgtgggcc	aggaagaccc	cgaggtcagt	ttcaactggg	acattgatgg	240
cgctgaggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgtaccg	300
cgtggtcagc	gtcctgcccc	tccagcacca	ggactggctg	acggggaagg	aattcaagtg	360
caagggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagaccggg	gagccgcagg	tgtacaccct	ggccccacac	cgggaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tgggtcaaagg	cttctaccca	cctgatatca	acgttgagtg	540
gcagaggaat	gggcagccgg	agtcagaggg	cacytacgcc	accacgccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	tgggtgatgca	cgaggccctg	cacaaccact	acaccagaa	720

<210> 6

<211> 248

<212> PRT

<213> Lama glama

<400> 6

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Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln
1          5          10          15
Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
          20          25          30
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
          35          40          45
Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp
          50          55          60
Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
65          70          75          80
Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
          85          90          95
Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
          100          105          110
Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
          115          120          125
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
          130          135          140
Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
145          150          155          160
Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
          165          170          175
Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
          180          185          190
Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
          195          200          205
Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
          210          215          220
Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
225          230          235          240
Ser Ile Thr Gln Ser Ser Gly Lys
          245

```

<210> 7

<211> 727

<212> DNA

<213> Lama glama

<400> 7

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caccggaaaa cctgaggtca cgtgcttggt gtggacgtgg gtaaagaaga ccctgagatc      180
gagttcaagc tgggtccgtgg atgacacaga ggtacacacg gctgagacaa agccaaagga      240
ggaacagttc aacagcacgt accgcgtggt cagcgtcctg cccatccagc accaggactg      300
gctgacgggg aaggaattca agtgcaaggt caacaacaaa gctctcccag ccccatcga      360
gaggaccatc tccaaggcca aagggcagac cggggagccg caggtgtaca ccctggcccc      420
acaccgggaa gagctggcca aggacaccgt gagegtaacc tgcttggtca aaggcttctt      480
cccagctgac atcaacgttg agtggcagag gaatgggag cgggagtcag agggcaccta      540
cgccaacacg ccgccacagc tggacaacga cgggacctac ttctctaca gaaactctc      600
cgtgggaaag aacacgtggc agcagggaga agtcttcacc tgtgtggtga tgcacgaggc      660
tctacacaat cactccaccc agaaatccat caccagctct tcgggtaaat agtaatctag      720

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<210> 8

<211> 236

<212> PRT

<213> Lama glama

<400> 8

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Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys
1          5          10          15
Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
          20          25          30
Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
          35          40          45
Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp
          50          55          60
Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
          65          70          75          80
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
          85          90          95
His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
          100          105          110
Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
          115          120          125
Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
          130          135          140
Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
          145          150          155          160
Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
          165          170          175
Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
          180          185          190
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
          195          200          205
Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
          210          215          220
Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
          225          230          235

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<210> 9

<211> 54

<212> DNA

<213> Homo sapiens

<400> 9

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54

<210> 10

<211> 18

<212> PRT

<213> Homo sapiens

<400> 10

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Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1          5          10          15
Pro Ala

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<210> 11

<211> 54

<212> DNA

<213> Homo sapiens
 <400> 11
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<210> 12
 <211> 18
 <212> PRT
 <213> Homo sapiens
 <400> 12
 Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 1 5 10 15
 Pro Ala

<210> 13
 <211> 327
 <212> DNA
 <213> Homo sapiens
 <400> 13
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 atgatctccc ggaccctga ggtcacatgc gtgggtggtg acgtgagcca cgaagaccct 120
 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180
 cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300
 atcgagaaaa ccattctcaa agccaaa 327

<210> 14
 <211> 109
 <212> PRT
 <213> Homo sapiens
 <400> 14
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 1 5 10 15
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 20 25 30
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 35 40 45
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 50 55 60
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 65 70 75 80
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 85 90 95
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105

<210> 15
 <211> 324
 <212> DNA
 <213> Homo sapiens
 <400> 15
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 aaccagggtca gectgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 120
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180
 gacggctcct tcttctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
 aacgtcttct catgtccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300
 ctctccctgt ccccggttaa atga 324

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<210> 16
<211> 107
<212> PRT
<213> Homo sapiens
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  1                               5               10               15
  Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                20                   25                   30
  Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                35                   40                   45
  Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
                50                   55                   60
  Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
  65                               70                   75                   80
  Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                               90                   95
  Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                100                   105

<210> 17
<211> 54
<212> DNA
<213> Homo sapiens
<400> 17
  gatcaggagc ccaaattcttc tgacaaaact cacacatccc caccgtcccc agca
                                                                54

<210> 18
<211> 18
<212> PRT
<213> Homo sapiens
<400> 18
  Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
  1                               5               10               15
  Pro Ala

<210> 19
<211> 712
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Synthetic
      nucleotide sequence
<400> 19
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  cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc      120
  ccggaccctt gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa      180
  gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga      240

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